

Appl. No. 09/889,053
Docket No. 7379M
Response to Non-Compliant Amendment dated October 17, 2006
Reply to Notice of Non-Compliant Amendment mailed on October 11, 2006
Customer No. 27752

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in this application:

1. (Currently amended) A method of ~~sequencing~~ determining an amino acid sequence of a polypeptide, said method comprising ~~comprising the steps of:~~

(a) providing the polypeptide, wherein the polypeptide comprises at least one N-terminus;

(b) providing a sulfonic acid;

(c) adding the sulfonic acid to the polypeptide, wherein said step produces a derivatized analyte; and

(d) analyzing said derivatized analyte using a mass spectrometric technique

~~(a) derivatizing a N terminus of a polypeptide or [[an]] a N termini of at least one peptide of the polypeptide with at least one acidic moiety having a pKa of less than about 2, when coupled with a polypeptide or at least one peptide of the polypeptide, to provide at least one derivatized analyte;~~

~~(b) analyzing the at least one derivatized analyte using a mass spectrometric technique to provide a fragmentation pattern; and~~

~~(c) interpreting the fragmentation pattern.~~

2. (Previously presented) The method recited in claim 1, wherein the mass spectrometric technique used is MALDI PSD mass spectrometry; or electrospray ionization tandem mass spectrometry.

Claims 3-7 (Canceled).

8. (Withdrawn) A kit for use in determining the amino acid sequence of a polypeptide characterized in that it comprises:

Appl. No. 09/889,053

Docket No. 7379M

Response to Non-Compliant Amendment dated October 17, 2006

Reply to Notice of Non-Compliant Amendment mailed on October 11, 2006

Customer No. 27752

(a) one or more acidic moiety reagents providing one or more acidic moieties having pK_as of less than 2 when coupled with the polypeptide or one or more peptides of the polypeptide; and

(b) means for derivatizing the N-terminus of the polypeptide or the N-termini of one or more peptides of the polypeptide with one or more acidic moiety reagents.

9. (Withdrawn) A kit according to Claim 8 characterized in that the means for derivatizing comprises one or more containment devices.

10. (Withdrawn) A kit according to Claim 9 characterized in that it further comprises one or more digestion aids.

11. (Currently amended) A method of sequencing determining an amino acid sequence of a polypeptide, said method comprising comprising the steps of:

(a) providing the peptide, wherein the peptide comprises at least one N-terminus;

(b) providing a sulfonic acid;

(c) adding the sulfonic acid to the peptide, wherein said step produces a derivatized analyte; and

(d) analyzing said derivatized analyte using a mass spectrometric technique adding at least one acidic group to the N terminus of a polypeptide or at least one peptide formed through cleavage of the polypeptide;

coupling the at least one acidic group to the N terminus, wherein said coupled polypeptide or at least one peptide has a pK_a of less than about 2;

providing at least one derivatized analyte with a mass spectra predominantly characterized by γ ions; and

analyzing the at least one derivatized analyte.

Appl. No. 09/889,053

Docket No. 7379M

Response to Non-Compliant Amendment dated October 17, 2006

Reply to Notice of Non-Compliant Amendment mailed on October 11, 2006

Customer No. 27752

12. (New) The method of claim 1, wherein said sulfonic acid comprises acid moieties chosen from 2-sulfoacetyl moiety, 3-sulfopropionyl moiety, 2-sulfobenzoyl moiety, and combinations thereof.

13. (New) The method of claim 11, wherein said sulfonic acid comprises acid moieties chosen from 2-sulfoacetyl moiety, 3-sulfopropionyl moiety, 2-sulfobenzoyl moiety, and combinations thereof.

14. (New) A method of determining an amino acid sequence of a polypeptide comprising the steps of:

a) providing the polypeptide, wherein the polypeptide comprises at least one N-terminus;

b) providing a derivatized analyte of the polypeptide;

c) providing an acidic moiety agent to the derivatized analyte to form a derivatized analyte complex, wherein said acidic moiety agent is chosen from dithiobis(sulfosuccinimidylpropionate), S-acetylmercaptosuccinic anhydride, 2-iminothiolane (which may also be referred to as Traut's reagent), dithiodiglycolic anhydride, tetrafluorosuccinic anhydride, hexafluoroglutaric anhydride, sulfosuccinic anhydride, 2-sulfobenzoic acid cyclic anhydride, chlorosulfonylacetyl chloride, and 1,3-propane sultone; and

d) analyzing said derivatized analyte complex.

15. (New) The method of claim 14, wherein said polypeptide is digested or cleaved to form at least two peptides.

16. (New) The method of claim 1, wherein said polypeptide is digested or cleaved to form at least two peptides.